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APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
09/714,865	11/16/2000	Diego H Castrillon	B0801/7195	4880

7590 06/18/2003

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EXAMINER	
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ART UNIT	PAPER NUMBER
1642	

DATE MAILED: 06/18/2003

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Please find below and/or attached an Office communication concerning this application or proceeding.

Office Action Summary

Application No.	Applicant(s)
09/714,865	Castrillon
Examiner	**Art Unit**
Karen Canella	1642

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE *3 months* MONTH(S) FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136 (a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If the period for reply specified above is less than thirty (30) days, a reply within the statutory minimum of thirty (30) days will be considered timely.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133).
- Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

Status

1) ☐ Responsive to communication(s) filed on _____.

2a) ☐ This action is FINAL. 2b) ☒ This action is non-final.

3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under ***Ex parte Quayle***, 1935 C.D. 11; 453 O.G. 213.

Disposition of Claims

4) ☒ Claim(s) *1-4 and 22* is/are pending in the application.

4a) Of the above, claim(s) _____ is/are withdrawn from consideration.

5) ☐ Claim(s) _____ is/are allowed.

6) ☒ Claim(s) *1, 3, 4, and 22* is/are rejected.

7) ☒ Claim(s) *2* is/are objected to.

8) ☐ Claims _____ are subject to restriction and/or election requirement.

Application Papers

9) ☐ The specification is objected to by the Examiner.

10) ☐ The drawing(s) filed on _____ is/are a) ☐ accepted or b) ☐ objected to by the Examiner.

Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).

11) ☐ The proposed drawing correction filed on _____ is: a) ☐ approved b) ☐ disapproved by the Examiner.

If approved, corrected drawings are required in reply to this Office action.

12) ☐ The oath or declaration is objected to by the Examiner.

Priority under 35 U.S.C. §§ 119 and 120

13) ☐ Acknowledgement is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).

a) ☐ All b) ☐ Some* c) ☐ None of:

1. ☐ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. _____.
3. ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

*See the attached detailed Office action for a list of the certified copies not received.

14) ☐ Acknowledgement is made of a claim for domestic priority under 35 U.S.C. § 119(e).

a) ☐ The translation of the foreign language provisional application has been received.

15) ☐ Acknowledgement is made of a claim for domestic priority under 35 U.S.C. §§ 120 and/or 121.

Attachment(s)

1) ☒ Notice of References Cited (PTO-892)
2) ☐ Notice of Draftsperson's Patent Drawing Review (PTO-948)
3) ☒ Information Disclosure Statement(s) (PTO-1449) Paper No(s). *6*
4) ☐ Interview Summary (PTO-413) Paper No(s). _____
5) ☐ Notice of Informal Patent Application (PTO-152)
6) ☐ Other:

DETAILED ACTION

1. Acknowledgment is made of applicants election of Group I, drawn to isolated nucleic acids and kits comprising agents which bind to isolated nucleic acids. Because applicant did not distinctly and specifically point out the supposed errors in the restriction requirement, the election has been treated as an election without traverse (MPEP § 818.03(a)).

2. Claims 12, 17, 25, 35, 47, 63, 66, 80 and 86-88 have been canceled. Claims 1-4 and 22 are pending and examined on the merits. Claim 22 is examined with this restriction group to the extent that it reads on kits comprising agents which bind to nucleic acids versus kits comprises agents which binds to proteins.

Claim Objections

3. Claim 3 is objected to under 37 CFR 1.75(c), as being of improper dependent form for failing to further limit the subject matter of a previous claim. Applicant is required to cancel the claim(s), or amend the claim(s) to place the claim(s) in proper dependent form, or rewrite the claim(s) in independent form. Claim 3 encompasses the isolated nucleic acid of SEQ ID NO:15 and fragments of SEQ ID NO:15. Claim 1 encompasses the nucleic acids which encode for human vasa protein encoded b SEQ ID NO:1. The fragments of SEQ ID NO:15 include a genus of nucleic acids which are not coextensive in scope with nucleic acids encoding the vasa protein of claim 1.

4. Claim 22 is objected to for recitation of an agent which selectively binds to an expression product of the nucleic acid of claim 1, which is a non-elected invention.

Claim Rejections - 35 USC § 112

5.The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

6. Claims 4 and 22 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claim 4 recites "unique fragments as set forth as SEQ ID NO:1 provided that the unique fragment includes a sequence of contiguous nucleotides which is not identical to any sequence selected from the group consisting of (1)sequences having the database accession numbers of Table 1, or sequences encoding a polypeptide having an amino acid sequence selected from the group consisting of SEQ ID NO:3, 4, 5, 6 or 7". The specification states on page 4, lines 22-24 that the unique fragment is of sufficient length to represent a sequence unique within the human genome. However, claim 4 states that the unique fragment must not be identical to a sequence of database accession numbers of Table I, or the sequences of SEQ D NO:3, 4, 5, 6, and 7, the complement or fragments of these sequences. The specification states on page 4, line 31 to page 5, line 8, that the sequence of contiguous nucleotides is selected from the group consisting of at least two contiguous nucleotides nonidentical to "the sequence group", at least three contiguous nucleotides non-identical to the "sequence group", etc. Thus, according to the specification the number of non-identical contiguous nucleotides can be as small as two. Lathe (J Mol Biol, 1985, Vol. 183, No. 1, pp. 1-12) teaches a minimum lengths of 16-18 nucleotides to define a unique fragment within a collection of expressed sequences from a single mammalian organism and a minimum length of 18-20 nucleotides to define a unique fragment within a single mammalian genome. These numbers are based on the estimated numbers of unique sequences in a cDNA library ($\sim 10^7$) versus a genomic library ($\sim 10^9$). It is unclear how a fragment which is of sufficient length to be unique within the genome of a mammalian organism can comprise a unique sequence of two nucleotides, based on the analysis of Lathe et al.

Claim 22 recites "a control for comparing to a measured value of binding of said agent". It is unclear what specific "measured value of binding" is referred to. Amendment of the claim to substitute ---a nucleic acid encoding the protein encoded by SEQ ID NO:1--- in place of "a

control for comparing to a measured value of binding of said agent to said isolated nucleic acid of claim 1 or expression product thereof" is recommended.

7.The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

8. Claims 1, 4 and 22 are rejected under 35 U.S.C. 112, first paragraph, as containing subject matter which was not described in the specification in such a way as to reasonably convey to one skilled in the relevant art that the inventor(s), at the time the application was filed, had possession of the claimed invention. Claim 1 is drawn to an isolated nucleic acid molecule selected from the group consisting of nucleic acid which hybridize under stringent conditions to a molecule consisting of a nucleic sequence set forth as SEQ ID NO:1 which code for a vasa polypeptide, and degenerate coding sequences and complements thereof. Claim 4 is drawn to an isolated nucleic acid molecule selected from unique fragments of SEQ ID NO:1. It is noted that claim 4 is rejected under 112, second paragraph for vague and indefinite language. The instant claims are drawn to polynucleotide sequences which hybridize under "stringent" conditions to SEQ ID NO:1 and complements of SEQ ID NO:1. The specification defines "stringent" conditions on page 11 lines 1-12 as encompassing washing of the membrane after hybridization with 0.1 X SSC or 0.1 SDS at temperatures up to 68 degrees. It is recognized in the art that low temperature wash conditions decrease the stringency of the hybridization. Thus, the conditions recited in the specification encompass low stringency and high stringency wash temperatures. The claim carries the limitation that the hybridizing polynucleotides must encode a vasa polypeptide, however, the specification defines a vasa polypeptide as being encoded by a nucleic acid which hybridizes to SEQ ID NO:1. The specification further contemplates that nucleic acids which encode a "respective human vasa polypeptide" having deletions and addition and substitutions to the vasa polypeptide encoded by the nucleic acids which hybridize to SEQ ID NO:2 are included in the present invention as vasa polypeptides (page 10, lines 18-22). The specification states that

human vasa is an isolated nucleic acid of SEQ ID NO:1 which codes for a protein which is specifically expressed in the gonads (page 9, line 23-25). The specification contemplates homologs and alleles of the human vasa nucleic acids as part of the instant invention which can be isolated by hybridization under stringent conditions to SEQ ID NO:1 (page 10, line 31 to page 11, line 12). The specification also contemplates variants of the human vasa which retain the function of the natural human vasa polypeptides as well as dominant-negative vasa polypeptides which do not retain the function of the natural human vasa polypeptide (page 20, lines 4-. Thus, when given the broadest reasonable interpretation, the claims drawn to hybridizing nucleic acids encompass not only degenerate coding sequences of SEQ ID NO:1, but homologs and alleles, variant and dominant-negative mutants of human vasa. It is concluded that the claims are drawn to a genus of nucleic acids which is highly variant as said genus encompasses polynucleotides encoding polypeptides having numerous structural and functional attributes. The specification describes human vasa polypeptide as SEQ ID NO:2 encoded by the polynucleotide of SEQ ID NO:1. The specification also describes SEQ ID NO:15 as comprising 13 additional nucleotides on the 5' end and 38 nucleotides on the 3' end of SEQ ID NO:1. The specification fails to describe mutational sites that exist in nature, and there is no description of how the structure of SEQ ID NO:1 relates to the structure of any strictly neutral alleles. The general knowledge in the art is that alleles are variant structures and the structure of one allele is not representative of unknown alleles. Further, the specification does not describe dominant negative mutants of seq id NO:1 or indicate where the mutation would be located. The general knowledge and skill in the art does not supplement the omitted description because specific, not general description is required. Thus, one of skill in the art would reasonably conclude that applicant did not disclose a representative number of species within the genus, as SEQ ID NO:1 does not sufficiently describe the claimed genus because of the structural and functional variation permitted within the genus. Thus, applicant was not in possession of the claimed genus.

Claim Rejections - 35 USC § 102

9. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

> A person shall be entitled to a patent unless -
>
> (b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

10. Claims 1 and 3 are rejected under 35 U.S.C. 102(b) as being anticipated by The New England Biolabs Catalog (1994, page 91). Claim 1 is drawn to an isolated nucleic acid molecule selected from the group consisting of nucleic acid which hybridize under stringent conditions to a molecule consisting of a nucleic sequence set forth as SEQ ID NO:1 which code for a vasa polypeptide, and degenerate coding sequences and complements thereof. Claim 3 is drawn to a fragment of SEQ ID NO:15.

The New England Biolabs Catalog discloses Random Primers on page 91 which would be complementary to the nucleic acids which hybridize under stringent conditions to seq id NO:1, or nucleic acid that differ in genetic code from said nucleic acids, thus fulfilling the specific embodiments of claim 1, section c. The random hexamers would be a fragment of seq id NO:15

11.. Claim 4 is rejected under 35 U.S.C. 102(b) as being anticipated by Hloch et al (Nucleic Acids Research, 1990, Vol. 18, page 3045) as evidenced by Lemaire et al (Life Sciences, 1993, Vol. 52, pp. 917-9260) and Castrillon et al (PNAS, 2000, Vol. 97, pp. 9585-9590) .

It is noted that the metes and bound of claim 4 cannot be determined for the reasons set forth in the rejection under 112, second paragraph, above.

Hloch et al disclose the polynucleotide and polypeptide sequence of human p68. Lemaire et al disclose that vasa and p68 and mouse PL10 share conserved protein segments(page 554, second column, under the heading "PL10 Deduced Protein Shares Similarities with Murine elF-

4A and Other Proteins"). Lemaire et al disclose that similarity between human p68 and other proteins encoding RNA helicases which are expressed within male germ cells is high in the region of the dead motif (table 1, page 921). Castrillon et al disclose that the human vasa gene contains a DEAD motif (page 9586, second column, lines 4-6 under the heading "Comparison of the Predicted Human VASA Protein Sequence with Other Species"). Thus, it is reasonable to conclude that the human p68 gene disclosed by Hloch et al comprises a DEAD motif having a unique fragment of SEQ ID NO:1. It is noted that murine p68, but not human p68 is excluded from claim 4.

12. Claim 2 is objected to as being dependent upon a rejected base claim, but would be allowable if rewritten in independent form including all of the limitations of the base claim and any intervening claims.

Conclusion

13. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Karen Canella whose telephone number is (703) 308-8362. The examiner can normally be reached on Monday through Friday from 8:30 am to 6:00 pm. A message may be left on the examiner's voice mail service. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Anthony Caputa, can be reached on (703) 308-3995. Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Karen A. Canella, Ph.D.

Patent Examiner, Group 1642

June 16, 2003